

RAW SEQUENCE LISTING

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Application Serial Number: 10/580,141
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/580,141

DATE: 04/20/2007
TIME: 11:19:31

Input Set : E:\10-580141.txt
Output Set: N:\CRF4\04202007\J580141.raw

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3 <110> APPLICANT: Aventis Pasteur Limited
4      Brunham, Robert
5      Raudonikiene, Ausra
6      Gallichan, Scott
7      Murdin, Andrew
9 <120> TITLE OF INVENTION: Immunization Against Chlamydia Infectio with 60K CRMP
11 <130> FILE REFERENCE: RY185
13 <140> CURRENT APPLICATION NUMBER: US 10/580,141
14 <141> CURRENT FILING DATE: 2006-05-19
16 <150> PRIOR APPLICATION NUMBER: US 60/481,676
17 <151> PRIOR FILING DATE: 2003-11-20
19 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/002004
20 <151> PRIOR FILING DATE: 2004-11-22
23 <160> NUMBER OF SEQ ID NOS: 14
25 <170> SOFTWARE: PatentIn version 3.3
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1662
29 <212> TYPE: DNA
30 <213> ORGANISM: Chlamydia muridium
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (1)..(1662)
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39 Met Arg Ile Gly Asp Pro Met Asn Lys Leu Ile Arg Arg Ala Val Thr
40 1          5           10          15
42 atc ttc gcg gtg act agt gtg gcg agt tta ttt gct agc ggg gtg tta      96
43 Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu
44          20          25          30
46 gag acc tct atg gca gag tct ctc tct acc aac gtt att agc tta gct      144
47 Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala
48          35          40          45
50 gac acc aaa gcg aaa gag acc act tct cat caa aaa gac aga aaa gca      192
51 Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala
52          50          55          60
54 aga aaa aat cat caa aat agg act tcc gta gtc cgt aaa gag gtt act      240
55 Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
56 65          70          75          80
58 gca gtt cgt gat act aaa gct gta gag cct aga cag gat tct tgc ttt      288
59 Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe
60          85          90          95
62 ggc aaa atg tat aca gtc aaa gtt aat gat gat cgt aat gta gaa atc      336
63 Gly Lys Met Tyr Thr Val Lys Val Asn Asp Arg Asn Val Glu Ile

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64	100	105	110	
66	gtg cag tcc gtt cct gaa tat gct acg gta gga tct cca tat cct att			384
67	Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile			
68	115	120	125	
70	gag att act gct ata ggg aaa aga gac tgt gtt gat gta atc att aca			432
71	Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr			
72	130	135	140	
74	cag caa tta cca tgc gaa gca gag ttt gtt agc agt gat cca gct act			480
75	Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr			
76	145	150	155	160
78	act cct act gct gat ggt aag cta gtt tgg aaa att gat cgg tta gga			528
79	Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly			
80	165	170	175	
82	cag ggc gaa aag agt aaa att act gta tgg gta aaa cct ctt aaa gaa			576
83	Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu			
84	180	185	190	
86	ggt tgc tgc ttt aca gct gca acg gtt tgt gct tgt cca gag atc cgt			624
87	Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg			
88	195	200	205	
90	tcg gtt acg aaa tgt ggc cag cct gct atc tgt gtt aaa cag gaa ggt			672
91	Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly			
92	210	215	220	
94	cca gaa agc gca tgt ttg cgt tgc cca gta act tat aga att aat gta			720
95	Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val			
96	225	230	235	240
98	gtc aac caa gga aca gca aca cgt aat gtt gtt gtg gaa aat cct			768
99	Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro			
100	245	250	255	
102	gtt cca gat ggc tat gct cat gca tcc gga cag cgt gta ttg aca tat			816
103	Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr			
104	260	265	270	
106	act ctt ggg gat atg caa cct gga gaa cag aga aca atc acc gtg gag			864
107	Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu			
108	275	280	285	
110	ttt tgt ccg ctt aaa cgt ggt cga gtc aca aat att gct aca gtt tct			912
111	Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser			
112	290	295	300	
114	tac tgt ggt gga cac aaa aat act gct acg gta aca aca gtg atc aat			960
115	Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn			
116	305	310	315	320
118	gag cct tgc gtg caa gtt aac atc gag gga gca gat tgg tct tat gtt			1008
119	Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val			
120	325	330	335	
122	tgt aag cct gta gaa tat gtt atc tct gtt tct aac cct ggt gac tta			1056
123	Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu			
124	340	345	350	
126	gtt tta cga gac gtt gta att gaa gat acg ctt tct cct gga ata act			1104
127	Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr			
128	355	360	365	

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gca gct gga gct cag att tct tgt aat aaa ttg gtt tgg	1152
Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp	
375 380	
gaa ctc aat cct gga gag tct tta caa tat aag gtt cta	1200
Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu	
390 395 400	
caa act cca ggg caa ttc aca aac aac gtt gtt gtg aaa	1248
Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys	
405 410 415	
gat tgc ggt att tgt act tct tgc gca gaa gca aca act	1296
Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr	
420 425 430	
gga gtt gct gct act cat atg tgc gta gta gat act tgt	1344
Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys	
440 445	
tgc gta gga gag aac act gtt tat cgt atc tgt gtg aca	1392
Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr	
455 460	
tct gct gaa gat aca aat gtg tcc tta att ttg aaa ttc	1440
Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe	
470 475 480	
tta caa cct ata tct ttc tct gga cca act aaa gga acc	1488
Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr	
485 490 495	
aac acg gta gtg ttt gat tcg tta cct aga tta ggt tct	1536
Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser	
500 505 510	
gta gag ttt tct gta acg ttg aaa gca gta tcc gct gga	1584
Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly	
520 525	
ggg gaa gct att ctt tct tcc gat aca ttg aca gtt cct	1632
Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro	
535 540	
acg gag aat aca cat atc tat	1662
Thr Glu Asn Thr His Ile Tyr	
550	
NO: 2	
I: 554	
PRT	
SM: Chlamydia muridium	
ICE: 2	
Gly Asp Pro Met Asn Lys Leu Ile Arg Arg Ala Val Thr	
5 10 15	
Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu	
20 25 30	
Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala	
40 45	
Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala	
55 60	

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202 Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr
 203 65 70 75 80
 206 Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe
 207 85 90 95
 210 Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile
 211 100 105 110
 214 Val Gln Ser Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile
 215 115 120 125
 218 Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr
 219 130 135 140
 222 Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr
 223 145 150 155 160
 226 Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly
 227 165 170 175
 230 Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu
 231 180 185 190
 234 Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg
 235 195 200 205
 238 Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly
 239 210 215 220
 242 Pro Glu Ser Ala Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val
 243 225 230 235 240
 246 Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro
 247 245 250 255
 250 Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr
 251 260 265 270
 254 Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu
 255 275 280 285
 258 Phe Cys Pro Leu Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser
 259 290 295 300
 262 Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn
 263 305 310 315 320
 266 Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val
 267 325 330 335
 270 Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu
 271 340 345 350
 274 Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr
 275 355 360 365
 278 Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp
 279 370 375 380
 282 Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu
 283 385 390 395 400
 286 Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys
 287 405 410 415
 290 Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr
 291 420 425 430
 294 Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys
 295 435 440 445
 298 Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr

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299	450	455	460	
302 Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe				
303 465	470	475	480	
306 Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr				
307	485	490	495	
310 Ile Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser				
311	500	505	510	
314 Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly				
315	515	520	525	
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322 Val Ser Asp Thr Glu Asn Thr His Ile Tyr				
323 545	550			
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334 <222> LOCATION: (1)..(1659)				
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339 1	5	10	15	
341 atc ttc gcg gtg act agt gtg gcg agt tta ttt gct agc ggg gtg tta				96
342 Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu				
343	20	25	30	
345 gag acc tct atg gca gag tct ctc tct aca aac gtt att agc tta gct				144
346 Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala				
347	35	40	45	
349 gac acc aaa gcg aaa gac aac act tct cat aaa agc aaa aaa gca aga				192
350 Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg				
351	50	55	60	
353 aaa aac cac agc aaa gag act ccc gta gac cgt aaa gag gtt gct ccg				240
354 Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro				
355 65	70	75	80	
357 gtt cat gag tct aaa gct aca gga cct aaa cag gat tct tgc ttt ggc				288
358 Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly				
359	85	90	95	
361 aga atg tat aca gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca				336
362 Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr				
363	100	105	110	
365 caa gct gtt cct gaa tat gct acg gta gga tct ccc tat cct att gaa				384
366 Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu				
367	115	120	125	
369 att act gct aca ggt aaa agg gat tgt gtt gat gtc att act cag				432
370 Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln				
371	130	135	140	
373 caa tta cca tgt gaa gca gag ttc gta cgc agt gat cca gcg aca act				480

VERIFICATION SUMMARY

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